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          35                      40                      45
Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
          50                      55                      60
Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
          65                      70                      75
Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
          80                      85                      90
Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
          95                     100                     105
Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
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Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
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Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
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Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu	155	160	165
Val Tyr Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe	170	175	180
Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser	185	190	195
Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly	200	205	210
Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly	215	220	225
Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly	230	235	240
Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu	245	250	255
Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln	260	265	270
Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu	275	280	285
Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala	290	295	300
Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys	305	310	315
Thr Tyr Ser Leu Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn	320	325	330
Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe	335	340	345
Asp Lys Ser Asn Pro Ile Leu Leu Arg Met Met Asn Asp Gln Leu	350	355	360
Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp	365	370	375
Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn	380	385	390
Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe	395	400	405

Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val
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425 430 435
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<210> 3
<211> 2653
<212> DNA
<213> *Homo sapiens*

<220>
<223> nucleotide sequence of human PSMA gene

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09973382-100901

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Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
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Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330

Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile	440	445	450
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Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu	485	490	495
Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro	500	505	510
Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe	515	520	525
Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn	530	535	540
Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val	545	550	555
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<213> Artificial sequence

<220>
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<210> 7
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<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<223> sense oligonucleotide primer based upon
intronic sequences of the PSMA genomic
clone used to amplify the corresponding
regions of the PSMA-like gene (exon 2)

<400> 7
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<210> 8
<211> 20
<212> DNA
<213> Artificial sequence

<220>
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<223> antisense oligonucleotide primer based upon
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clone used to amplify the corresponding
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<400> 8
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<210> 9
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<212> DNA
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<220>
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<223> sense oligonucleotide primer based upon
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clone used to amplify the corresponding
regions of the PSMA-like gene (exon 3)

<400> 9
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<210> 10
<211> 22
<212> DNA
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<220>
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<400> 10
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<210> 11
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<210> 12
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<220>
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<210> 13
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<210> 14
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<400> 14
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<210> 15
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<210> 16
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 <400> 16
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 <210> 17
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 <210> 18
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 <212> DNA
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 <220>
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 <400> 18
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<210> 20
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<400> 20
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<210> 21
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<210> 22
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<400> 22
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<210> 23
<211> 22
<212> DNA
<213> Artificial sequence

<220>
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<210> 24
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<210> 25
<211> 22
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<220>
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<400> 25
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<210> 26
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<210> 27
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<210> 28
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<220>
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<210> 29
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<220>
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<210> 30
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <221> primer_bind
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 clone used to amplify the corresponding
 regions of the PSMA-like gene (exon 15)

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<210> 31
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 <212> DNA
 <213> Artificial sequence

<220>
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<210> 32
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 <212> DNA
 <213> Artificial sequence

<220>
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 regions of the PSMA-like gene (exons 16-17)

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<210> 33
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clone used to amplify the corresponding
regions of the PSMA-like gene (exon 19)

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